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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=1; day=6; hr=14; min=22; sec=50; ms=92;]

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Application No: 10522106

Version No: 3.0

Input Set:

Output Set:

Started: 2009-12-15 16:22:28.242
Finished: 2009-12-15 16:22:35.214
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 972 ms
Total Warnings: 14
Total Errors: 66
No. of SeqIDs Defined: 36
Actual SeqID Count: 36

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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (17)
E 300	Invalid codon found Thr SEQID (17) POS: 1153
E 300	Invalid codon found Ala SEQID (17) POS: 1156
E 300	Invalid codon found Val SEQID (17) POS: 1159
E 300	Invalid codon found His SEQID (17) POS: 1162
E 300	Invalid codon found Thr SEQID (17) POS: 1165
E 300	Invalid codon found Leu SEQID (17) POS: 1168
E 300	Invalid codon found Ala SEQID (17) POS: 1171
E 300	Invalid codon found His SEQID (17) POS: 1174
E 300	Invalid codon found Val SEQID (17) POS: 1177
E 300	Invalid codon found Thr SEQID (17) POS: 1180
E 300	Invalid codon found Cys SEQID (17) POS: 1183
E 300	Invalid codon found Asp SEQID (17) POS: 1186
E 300	Invalid codon found Phe SEQID (17) POS: 1189
E 300	Invalid codon found Pro SEQID (17) POS: 1192
E 300	Invalid codon found Arg SEQID (17) POS: 1195
E 300	Invalid codon found Leu SEQID (17) POS: 1198
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)

Input Set:

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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)

SEQUENCE LISTING

<110> Kogel, Karl-Heinz
Huckelhoven, Ralph
Trujillo, Marco

<120> Method for Obtaining a Pathogen Resistance in Plants

<130> 12810-00067-US

<140> 10522106

<141> 2009-12-15

<150> PCT/EP03/07589

<151> 2003-07-14

<150> DE 10233327.0

<151> 2002-07-22

<160> 36

<170> PatentIn Ver. 3.3

<210> 1

<211> 337

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (2)..(337)

<223> coding for NADPH oxidase (fragment)

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Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile

1 5 10 15

att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct 97

Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Asp Ala

20 25 30

cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat 145

Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn

35 40 45

ggt gtc gat gta gtg tct ggm act cga gtc cgg aca cat ttt gca aga 193

Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg

50 55 60

cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat 241

Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr

65 70 75 80

gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa 289

Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu

85 90 95

cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc 337

Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe

100 105 110

<210> 2

<211> 112

<212> PRT

<213> Hordeum vulgare

<220>

<221> misc_feature

<222> (55)..(55)

<223> The 'Xaa' at location 55 stands for Gly.

<400> 2

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1 5 10 15
Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
20 25 30
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
35 40 45
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
50 55 60
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
65 70 75 80
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
85 90 95
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe
100 105 110

<210> 3

<211> 2832

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(2829)

<223> coding for NADPH oxidase

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1 5 10 15
acg aca ccg cgg tcg ctg acg acg ggc tcg tcg ccg cgc ggg tcc gac 96
Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp
20 25 30
gac cgg agc tcc gac gac ggg gag gag ctg gtc gag gtc acg ctc gac 144
Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp
35 40 45
ctg cag gac gac acc att gtg ctt cgg agc gtc gag ccc gcg gcg 192
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala
50 55 60
gcg gcg gcg ggg gtg ggg gcg ggg gcg ggg gcg gcg tcg gcg cgg 240
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Ala Ser Ala Arg
65 70 75 80
ggg gag ctc acg ggt ggc ccg tcg tcg tcg tcg cgg tcg agg tcg 288
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Arg Ser Arg Ser
85 90 95
ccg tcg atc cgg agg agc tcg tcg cac cgg ctg ctg cag ttc tcg cag 336
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln
100 105 110
gag ctc aag gcg gag gcc atg gcc cgg gcg cgg cag ttc tcg cag gac 384

Glu	Leu	Lys	Ala	Glu	Ala	Met	Ala	Arg	Ala	Arg	Gln	Phe	Ser	Gln	Asp	
115				120							125					
ctg	acc	aag	cgg	tcc	ggc	cgc	agc	cac	agc	cgc	agc	gaa	gcg	cag	gcg	432
Leu	Thr	Lys	Arg	Phe	Gly	Arg	Ser	His	Ser	Arg	Ser	Glu	Ala	Gln	Ala	
130				135							140					
cgc	tgc	ggc	ctc	gag	tcc	gcf	ctc	gcc	cgc	gcc	gcf	cgg	cgg	cag		480
Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln	
145				150						155				160		
cgc	gcf	cag	ctc	gac	cgc	aca	cgc	tcc	ggc	gcc	cac	aag	gcf	ctc	cgc	528
Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Gly	Ala	His	Lys	Ala	Leu	Arg	
165				170						175						
ggc	ctc	cgc	tcc	atc	agc	agc	aac	aag	gcc	aac	aac	gcc	tgg	atg	gag	576
Gly	Leu	Arg	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Asn	Asn	Ala	Trp	Met	Glu	
180				185						190						
gtg	cag	gcc	aac	tcc	gac	cgc	ctc	gcc	cgc	gac	ggc	tac	ctc	tcc	cgc	624
Val	Gln	Ala	Asn	Phe	Asp	Arg	Leu	Ala	Arg	Asp	Gly	Tyr	Ley	Ser	Arg	
195				200						205						
tcc	gac	tcc	gcc	gaa	tgc	atc	ggg	atg	acg	gaa	tcg	aag	gag	tcc	gcf	672
Ser	Asp	Phe	Ala	Glu	Cys	Ile	Gly	Met	Thr	Glu	Ser	Lys	Glu	Phe	Ala	
210				215						220						
ctc	gag	ctg	tcc	gac	acg	ctg	agc	cgg	cga	cga	cag	atg	aag	gtg	gac	720
Leu	Glu	Leu	Phe	Asp	Thr	Leu	Ser	Arg	Arg	Arg	Gln	Met	Lys	Val	Asp	
225				230						235				240		
acg	att	aac	aag	gat	gaa	ctc	cgc	gag	atc	tgg	cag	cag	atc	acc	gat	768
Thr	Ile	Asn	Lys	Asp	Glu	Leu	Arg	Glu	Ile	Trp	Gln	Gln	Ile	Thr	Asp	
245				250						255						
aac	agc	tcc	gac	tcc	cgt	ctc	caa	atc	tcc	tcc	gaa	atg	gtg	gtt	aat	816
Asn	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Glu	Met	Val	Asp	Lys	
260				265						270						
aac	gcf	gac	ggc	cgg	att	acg	gag	gcf	gag	gtg	aaa	gag	att	att	atg	864
Asn	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Ala	Glu	Val	Lys	Glu	Ile	Ile	Met	
275				280						285						
ttg	agc	gcf	tct	gcc	aat	aaa	ctg	tcg	agg	ctt	aag	gag	caa	gca	gaa	912
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	
290				295						300						
gag	tac	gcc	gct	ttg	atc	atg	gag	gag	ctt	gat	cct	gaa	ggg	ctc	ggc	960
Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Gly	Leu	Gly	
305				310						315				320		
tac	att	gag	cta	tgg	caa	ttg	gag	aca	ctt	ctg	ttg	cag	aaa	gat	acc	1008
Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Gln	Lys	Asp	Thr		
325				330						335						
tat	atg	aac	tat	agt	cag	gcc	ctt	agt	tac	aca	agc	caa	gca	ctg	agc	1056
Tyr	Met	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	
340				345						350						
cag	aat	ctt	gca	ggg	cta	agg	aag	aag	agt	tca	atc	cgc	aaa	ata	agc	1104
Gln	Asn	Leu	Ala	Gly	Leu	Arg	Lys	Lys	Ser	Ser	Ile	Arg	Lys	Ile	Ser	
355				360						365						
acc	tct	tta	agc	tac	tat	tcc	gag	gac	aac	tgg	aaa	cgt	tta	tgg	gtg	1152
Thr	Ser	Leu	Ser	Tyr	Tyr	Phe	Glu	Asp	Asn	Trp	Lys	Arg	Leu	Trp	Val	
370				375						380						
ctt	gca	ttg	tgg	att	ggg	ata	atg	gct	gga	ctg	tcc	acc	tgg	aaa	tcc	1200
Leu	Ala	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe	
385				390						395				400		
atg	cag	tat	cgt	aac	cga	tat	gtc	ttt	gat	gtg	atg	ggc	tac	tgt	gtc	1248
Met	Gln	Tyr	Arg	Asn	Arg	Tyr	Val	Phe	Asp	Val	Met	Gly	Tyr	Cys	Val	
405				410						415						
aca	aca	gca	aaa	gga	gct	gct	gaa	acc	cta	aag	ctg	aat	atg	gca	att	1296

Thr Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu Asn Met Ala Ile			
420	425	430	
atc ctc ctg cca gta tgc cgt aac acc att act tgg ttg cga agt aca			1344
Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Ser Thr			
435	440	445	
agg gct gca cg gca cta cct ttt gat gac aac atc aac ttc cac aag			1392
Arg Ala Ala Arg Ala Leu Pro Phe Asp Asp Asn Ile Asn Phe His Lys			
450	455	460	
act att gca gca gca att gtg gtt ggt ata atc ctc cat gca ggg aac			1440
Thr Ile Ala Ala Ala Ile Val Val Gly Ile Ile Leu His Ala Gly Asn			
465	470	475	480
cac ctt gta tgc gat ttt cca cgg tta ata aaa tca tca gat gag aag			1488
His Leu Val Cys Asp Phe Pro Arg Leu Ile Lys Ser Ser Asp Glu Lys			
485	490	495	
tat gct cct ttg ggc cag tat ttt ggg gaa ata aag cca aca tat ttt			1536
Tyr Ala Pro Leu Gly Gln Tyr Phe Gly Glu Ile Lys Pro Thr Tyr Phe			
500	505	510	
aca ttg gtc aaa gga gtg gag ggc atc act ggg gta atc atg gtt gta			1584
Thr Leu Val Lys Gly Val Glu Gly Ile Thr Gly Val Ile Met Val Val			
515	520	525	
tgc atg ata att gct ttt act cta gca acc cgg tgg ttc cgc cgt agc			1632
Cys Met Ile Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser			
530	535	540	
ttg gtt aag ctt cca agg cca ttt gac aaa ctg act ggc ttc aat gcc			1680
Leu Val Lys Leu Pro Arg Pro Phe Asp Lys Leu Thr Gly Phe Asn Ala			
545	550	555	560
ttt tgg tat tct cat cat ctg ttc atc att gtg tat atc gcg ctc att			1728
Phe Trp Tyr Ser His His Leu Phe Ile Ile Val Tyr Ile Ala Leu Ile			
565	570	575	
gtt cat gga gag tgt cta tac ctt att cat gtc tgg tac aga aga acg			1776
Val His Gly Glu Cys Leu Tyr Leu Ile His Val Trp Tyr Arg Arg Thr			
580	585	590	
aca tgg atg tat ctt tca gtc cct gtt tgc ttg tat gta ggg gag agg			1824
Thr Trp Met Tyr Leu Ser Val Pro Val Cys Leu Tyr Val Gly Glu Arg			
595	600	605	
att cta agg ttc ttc agg tct ggc agt tat tct gtc cgg cta ttg aag			1872
Ile Leu Arg Phe Phe Arg Ser Gly Ser Tyr Ser Val Arg Leu Leu Lys			
610	615	620	
gtg gcc ata tat cca ggt aat gtt ttg aca ctg caa atg tcc aag cct			1920
Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro			
625	630	635	640
ccc acg ttc cgt tac aag agt gga caa tat atg ttt gtt caa tgt cca			1968
Pro Thr Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro			
645	650	655	
gca gtg tct ccc ttt gaa tgg cat ccc ttc tca att act tca gca cct			2016
Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro			
660	665	670	
ggg gat gac tac ctc agc att cat gtt cga caa ctt ggt gat tgg aca			2064
Gly Asp Asp Tyr Leu Ser Ile His Val Arg Gln Leu Gly Asp Trp Thr			
675	680	685	
cga gaa ctc aag aga gta ttt gct gca gct tgt gag ccc cca gcg ggt			2112
Arg Glu Leu Lys Arg Val Phe Ala Ala Ala Cys Glu Pro Pro Ala Gly			
690	695	700	
ggt aaa agc ggc ctt ctt agg gca gat gag aca act aag aaa atc tta			2160
Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Thr Thr Lys Lys Ile Leu			
705	710	715	720
ccc aag ctt ctg att gat gga ccg tat ggt tct cct gct cag gat tac			2208

Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ser Pro Ala Gln Asp Tyr			
725	730	735	
agc aag tat gat gtt tta tta ctt gtt gga tta gga att ggt gcg aca			2256
Ser Lys Tyr Asp Val Leu Leu Leu Val Gly Leu Gly Ile Gly Ala Thr			
740	745	750	
ccc ttt att agc ata tta aaa gat ctt ctg aat aac atc atc aaa atg			2304
Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Ile Lys Met			
755	760	765	
gag gaa gag gag gat gct tct act gat ctt tat cca cca atg ggt cggt			2352
Glu Glu Glu Asp Ala Ser Thr Asp Leu Tyr Pro Pro Met Gly Arg			
770	775	780	
aat aag cca cat gtt gat ctg ggc aca ctt atg acg att acc tca aga			2400
Asn Lys Pro His Val Asp Leu Gly Thr Leu Met Thr Ile Thr Ser Arg			
785	790	795	800
cca aag aag atc ttg aag acc aca aat gct tac ttt tac tgg gtg aca			2448
Pro Lys Lys Ile Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr			
805	810	815	
cgt gag caa ggc tct ttt gat tgg ttc aaa gga gtc atg aat gaa att			2496
Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Ile			
820	825	830	
gct gac ttg gat caa agg aat atc att gag atg cac aac tac cta aca			2544
Ala Asp Leu Asp Gln Arg Asn Ile Ile Glu Met His Asn Tyr Leu Thr			
835	840	845	
agc gtc tat gag gag ggg gat gcc agg tca gca ctc atc acc atg ctc			2592
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu			
850	855	860	
caa gct ctg aac cat gcc aag aat gga gtt gat att gtc tct ggg aca			2640
Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr			
865	870	875	880
aaa gtc cgg aca cat ttt gca cga cca aat tgg aga aag gtc ctt tct			2688
Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser			
885	890	895	
aaa att tcc tcc aag cat cca tat gcc aaa ata ggt gta ttc tac tgt			2736
Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys			
900	905	910	
gga gct cca gtc ctg gca caa gaa cta agc aaa ctt tgc cat gaa ttc			2784
Gly Ala Pro Val Leu Ala Gln Glu Leu Ser Lys Leu Cys His Glu Phe			
915	920	925	
aac ggg aaa tgc aca acg aag ttc gaa ttc cat aag gag cat ttc tga			2832
Asn Gly Lys Cys Thr Thr Lys Phe Glu Phe His Lys Glu His Phe			
930	935	940	

<210> 4

<211> 943

<212> PRT

<213> Oryza sativa

<400> 4

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20	25	30	

Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp			
35	40	45	

Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala			
50	55	60	

Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg
65 70 75 80
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Ser Arg Ser Arg Ser
85 90 95
Pro Ser Ile Arg Arg Ser Ser His Arg Leu Leu Gln Phe Ser Gln
100 105 110
Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp
115 120 125
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala
130 135 140
Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Ala Arg Arg Gln
145 150 155 160
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg
165 170 175
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu
180 185 190
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg
195 200 205
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala
210 215 220
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Gln Met Lys Val Asp
225 230 235 240
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp
245 250 255
Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys
260 265 270
Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met
275 280 285
Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu
290